Species *Blautia aquisgranensis*

Etymology

[a.quis.gra.nen'sis] **N.L. fem. adj.** *aquisgranensis*, named after the German city of Aachen (Latin name Aquisgranum) where it was isolated

Nomenclatural type

Strain: CLA JM-H16 = DSM 114586 = LMG 33033

Description

The genome size is 3.63 Mbp, G+C percentage is 43.76%, with 99.37% completeness and 0.32% contamination. It includes two plasmids (37,495 bp; 1,036 bp). The closest relative to strain CLA-JM-H16 was Blautia intestinalis (96.11%) based on 16S rRNA gene analysis. Placement of the strain within Blautia was confirmed based on POCP comparison as values above 50% to multiple Blautia species were obtained. However, comparison to the type species of the genus, Blautia coccoides, gave a value of 42.36%. This inconsistency was also highlighted by GTDB-Tk, which classified strain CLA-JM-H16 as 'Blautia_A sp900764225', suggesting Blautia may require splitting into multiple genera in future. As the separation of Blautia would require detailed analysis which is outside the scope of this manuscript, we propose strain CLA-JM-H16 as a novel species within Blautia. All three novel species of Blautia described within this manuscript were confirmed to represent distinct species based on ANI comparison (B. aquisgranensis Vs. B. caccae, 81.74%; B. aquisgranensis Vs. B. intestinihominis, 76.95%; B. caccae Vs. B. intestinihominis, 78.57%). Functional analysis revealed 157 transporters, 17 secretion genes, and predicted utilization of arbutin, salicin, sucrose, starch, and production of acetate, propionate, folate, L-glutamate, riboflavin, and cobalamin. In total, 205 CAZymes were identified, with 40 different glycoside hydrolase families and 12 glycoside transferase families represented. The strain CLA-JM-H16 (phylum Bacillota, family Lachnospiraceae) was isolated from human faeces.

Classification

Bacteria » *Bacillota* » *Clostridia* » *Lachnospirales* » *Lachnospiraceae* » *Blautia* » *Blautia aquisgranensis*

References

Effective publication: Hitch et al., 2025 [1]

Registry URL

https://seqco.de/i:48043

References

1. Hitch et al. (2025). HiBC: a publicly available collection of bacterial strains isolated from the human gut. *Nature Communications*. DOI:10.1038/s41467-025-59229-9